

05/90  
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#3



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## RAW SEQUENCE LISTING

DATE: 02/24/2003

PATENT APPLICATION: US/09/770,564

TIME: 10:15:32

Input Set : N:\Crf3\RULE60\09770564.raw.txt  
 Output Set: N:\CRF4\02242003\I770564.raw

4 <110> APPLICANT: Crasta, Oswald R.  
 5 Duvick, Jonathan P.  
 6 Folkerts, Otto  
 7 Gilliam, Jacob T.  
 8 Maddox, Joyce R.  
 11 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase  
 12 Polynucleotides and Related Polypeptides and Methods of Use  
 15 <130> FILE REFERENCE: 0875  
 17 <140> CURRENT APPLICATION NUMBER: US 09/770,564  
 18 <141> CURRENT FILING DATE: 2001-01-26  
 20 <150> PRIOR APPLICATION NUMBER: US 09/352,168  
 21 <151> PRIOR FILING DATE: 1999-07-12  
 23 <150> PRIOR APPLICATION NUMBER: 60/092,936  
 24 <151> PRIOR FILING DATE: 1998-07-25  
 26 <160> NUMBER OF SEQ ID NOS: 33  
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 372  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Exophiala spinifera.  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: misc\_feature  
 37 <222> LOCATION: (346)...(346)  
 38 <223> OTHER INFORMATION: n = A,T,C or G  
 40 <400> SEQUENCE: 1  
 41 gggccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgcgtaccc 60  
 42 gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc 120  
 43 attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180  
 44 ggaggacgcc cgagaaggct tggcgcgcc accacggctt gtcccatatcg aagactatct 240  
 45 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgcc ggaagagggt 300  
 W--> 46 gtgaaaatgt caaggtggga tacaagggttgc tcggtaacga aaccancacc ttttgcttc 360  
 47 ggaacacggc gc 372  
 49 <210> SEQ ID NO: 2  
 50 <211> LENGTH: 182  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Exophiala spinifera.  
 54 <400> SEQUENCE: 2  
 55 gaattttccg ccaatgcttg cttctcgccg ggaagagggtg gtgaaaatgt caaggtggga 60  
 56 tacaagggttgc tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccgaggcc 120  
 57 gatcgactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180  
 58 ac 182  
 60 <210> SEQ ID NO: 3  
 61 <211> LENGTH: 29

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Input Set : N:\Crf3\RULE60\09770564.raw.txt  
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62 <212> TYPE: DNA  
 63 <213> ORGANISM: Artificial Sequence  
 65 <220> FEATURE:  
 66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965  
 68 <400> SEQUENCE: 3  
 69 tggtttcgtt accgacaacc ttgtatccc 29  
 71 <210> SEQ ID NO: 4  
 72 <211> LENGTH: 28  
 73 <212> TYPE: DNA  
 74 <213> ORGANISM: Artificial Sequence  
 76 <220> FEATURE:  
 77 <223> OTHER INFORMATION: Desiged oligonucleotide for 5' RACE, N21968  
 79 <400> SEQUENCE: 4  
 80 gagtttgtcc cagacagact tttgtcgt 28  
 82 <210> SEQ ID NO: 5  
 83 <211> LENGTH: 1389  
 84 <212> TYPE: DNA  
 85 <213> ORGANISM: Exophiala spinifera  
 87 <220> FEATURE:  
 88 <221> NAME/KEY: CDS  
 89 <222> LOCATION: (1)...(1386)  
 91 <400> SEQUENCE: 5  
 92 gac aac gtt gcg gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg 48  
 93 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu  
 94 1 5 10 15  
 96 gag acg gca cgc aaa gtc cag gcc gtc ggt ctg tcc tgc ctc gtt ctt 96  
 97 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
 98 20 25 30  
 100 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
 101 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 102 35 40 45  
 104 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
 105 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 106 50 55 60  
 108 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
 109 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 110 65 70 75 80  
 112 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
 113 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
 114 85 90 95  
 116 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
 117 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
 118 100 105 110  
 120 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
 121 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
 122 115 120 125  
 124 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432  
 125 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
 126 130 135 140

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128	ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
129	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
130	145 150 155 160	
132	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
133	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
134	165 170 175	
136	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
137	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
138	180 185 190	
140	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
141	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
142	195 200 205	
144	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
145	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
146	210 215 220	
148	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
149	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
150	225 230 235 240	
152	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
153	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
154	245 250 255	
156	gcc gtg ttc cga agc aaa aag gtg gtt tcg tta ccg aca acc ttg	816
157	Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu	
158	260 265 270	
160	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
161	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
162	275 280 285	
164	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
165	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
166	290 295 300	
168	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
169	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
170	305 310 315 320	
172	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
173	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
174	325 330 335	
176	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
177	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
178	340 345 350	
180	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
181	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
182	355 360 365	
184	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
185	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
186	370 375 380	
188	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
189	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
190	385 390 395 400	
192	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248

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193 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
194 405 410 415  
196 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg 1296  
197 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
198 420 425 430  
200 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa 1344  
201 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
202 435 440 445  
204 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1386  
205 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
206 450 455 460  
208 tag 1389  
210 <210> SEQ ID NO: 6  
211 <211> LENGTH: 462  
212 <212> TYPE: PRT  
213 <213> ORGANISM: Exophiala spinifera  
215 <400> SEQUENCE: 6  
216 Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu  
217 1 5 10 15  
218 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
219 20 25 30  
220 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
221 35 40 45  
222 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
223 50 55 60  
224 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
225 65 70 75 80  
226 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
227 85 90 95  
228 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
229 100 105 110  
230 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
231 115 120 125  
232 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
233 130 135 140  
234 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
235 145 150 155 160  
236 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
237 165 170 175  
238 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
239 180 185 190  
240 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
241 195 200 205  
242 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
243 210 215 220  
244 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
245 225 230 235 240  
246 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
247 245 250 255

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Output Set: N:\CRF4\02242003\I770564.raw

248 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
 249 260 265 270  
 250 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
 251 275 280 285  
 252 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
 253 290 295 300  
 254 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
 255 305 310 315 320  
 256 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
 257 325 330 335  
 258 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
 259 340 345 350  
 260 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
 261 355 360 365  
 262 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
 263 370 375 380  
 264 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
 265 385 390 395 400  
 266 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
 267 405 410 415  
 268 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
 269 420 425 430  
 270 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
 271 435 440 445  
 272 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 273 450 455 460

275 &lt;210&gt; SEQ ID NO: 7

276 &lt;211&gt; LENGTH: 1442

277 &lt;212&gt; TYPE: DNA

278 &lt;213&gt; ORGANISM: Exophiala spinifera

280 &lt;220&gt; FEATURE:

281 &lt;221&gt; NAME/KEY: CDS

282 &lt;222&gt; LOCATION: (1)...(646)

284 &lt;221&gt; NAME/KEY: intron

285 &lt;222&gt; LOCATION: (647)...(699)

W--&gt; 287 &lt;221&gt; CDS

288 &lt;222&gt; LOCATION: (700)...(1439)

W--&gt; 290 &lt;400&gt; 7

291 gac aac gtt gcg gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg 48  
 292 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu  
 293 1 5 10 15  
 295 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96  
 296 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
 297 20 25 30  
 299 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
 300 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 301 35 40 45  
 303 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
 304 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/24/2003  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346

## Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings. Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:18,20,24,25,26,27,28,29,30,31,32,33

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300  
 L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
 L:290 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
 L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
 L:802 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16  
 L:1044 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
 L:1048 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
 L:1052 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
 L:1343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
 L:1350 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
 L:1351 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
 L:1353 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
 L:1357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
 L:1816 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:1820 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:1824 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:1828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:1832 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:1835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:1839 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
 L:2102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>

ORGANISM:Unknown

L:2102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:2102  
 L:2240 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:2244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2259 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
 L:2523 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>

ORGANISM:Unknown

L:2523 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2523  
 L:2660 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:2663 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2667 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2671 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2675 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2679 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2683 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
 L:2994 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>

ORGANISM:Unknown

L:2994 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>  
 ORGANISM:Unknown  
 L:2994 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2994  
 L:3158 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
 L:3159 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
 L:3161 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
 L:3165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
 L:3169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
 L:3173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
 L:3177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30

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Input Set : N:\Crf3\RULE60\09770564.raw.txt  
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L:3180 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3491 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>  
ORGANISM:Unknown  
L:3491 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>  
ORGANISM:Unknown  
L:3491 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:3491  
L:3654 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:3657 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3661 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3665 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3669 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3673 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3888 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>  
ORGANISM:Unknown